Amendments to the Claims:

1. (Currently amended) A method to inactivate a nucleotide sequence of interest introduced into a genome of a plant cell, said method comprising:

transforming said plant cell with a nucleic acid molecule comprising a promoter operably linked to a said nucleotide sequence of interest; and

introducing into said plant cell at least one chimeric oligonucleotide, said chimeric oligonucleotide having at least a first block of RNA residues and a second block of RNA residues, wherein said first and said second ~~blocks~~ block of RNA residues are homologous to said nucleic acid molecule ~~and~~ ; said first and said second block of RNA residues are about 3 nucleotides to about 20 nucleotides in length and are contiguous with and flank a block of DNA residues, wherein the block of DNA residues comprises at least one mismatch to the nucleic acid molecule and said block of DNA residues is about 5 nucleotides to about 60 nucleotides in length; wherein said first RNA block, said DNA block and said second RNA block are identical to a contiguous sequence of the nucleic acid molecule except for the presence of said mismatch in said DNA block; ~~and~~ said chimeric oligonucleotide comprises additional DNA residues that are capable of forming a duplex structure with said first block of RNA residues, said block of DNA residues, and said second block of RNA residues; and, said chimeric oligonucleotide being capable of recognizing and implementing a nucleotide conversion in said nucleic acid molecule.

2. (Original) The method of claim 1, wherein said nucleotide conversion is in the promoter.

3. (Previously presented) The method of claim 1, wherein said nucleotide conversion is in a coding region of said nucleotide sequence of interest.

4. (Previously presented) The method of claim 1, wherein said nucleotide sequence of interest comprises a selectable marker.

5. (Previously presented) The method of claim 1, wherein said nucleotide sequence of interest modifies herbicide resistance.

6. (Previously presented) The method of claim 1, wherein the chimeric oligonucleotide introduces a frameshift in the normal reading frame of the nucleotide sequence of interest.

7. (Previously presented) The method of claim 1, wherein the chimeric oligonucleotide introduces a premature stop codon in the normal reading frame of the nucleotide sequence of interest.

8. (Previously presented) The method of claim 2, wherein the chimeric oligonucleotide introduces a modification in a region of the promoter critical for transcription of the operably linked nucleotide sequence of interest.

9. (Previously presented) The method of claim 5, wherein said nucleotide sequence of interest encodes 5-enol pyruvylshikimate-3-phosphate synthase.

10. (Previously presented) The method of claim 5, wherein said nucleotide sequence of interest encodes acetohydroxy acid synthetase.

11. (Previously presented) The method of claim 9, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10.

12. (Previously presented) The method of claim 10, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 11, 12, and 13.

13. (Previously presented) The method of claim 1, wherein said plant cell is from a monocot.

14. (Previously presented) The method of claim 13, wherein said monocot is maize.

15. (Previously presented) The method of claim 1, wherein said plant cell is from a dicot.

16. (Currently amended) A method to inactivate a nucleotide sequence of interest introduced into a genome of a plant, said method comprising:

transforming said plant with a nucleic acid molecule comprising a promoter operably linked to ~~a~~ said nucleotide sequence;

introducing into said plant at least one chimeric oligonucleotide, said chimeric oligonucleotide having at least a first block of RNA residues and a second block of RNA residues, wherein said first and said second ~~blocks~~ block of RNA residues are homologous to said nucleic acid molecule ~~and~~ ; said first and said second block of RNA residues are about 3 nucleotides to about 20 nucleotides in length and are contiguous with and flank a block of DNA residues, wherein the block of DNA residues comprises at least one mismatch to the nucleic acid molecule and said block of DNA residues is about 5 nucleotides to about 60 nucleotides in length; wherein said first RNA block, said DNA block and said second RNA block are identical to a contiguous sequence of the nucleic acid molecule except for the presence of said mismatch in said DNA block; ~~and~~ said chimeric oligonucleotide comprises additional DNA residues that are capable of forming a duplex structure with said first block of RNA residues, said block of DNA residues, and said second block of RNA residues; and, said chimeric oligonucleotide being capable of recognizing and implementing a nucleotide conversion in said nucleic acid molecule.

17. (Previously presented) The method of claim 16, wherein said nucleotide conversion is in the promoter.

18. (Previously presented) The method of claim 16, wherein said nucleotide conversion is in a coding region of said nucleotide sequence of interest.

19. (Previously presented) The method of claim 16, wherein the chimeric oligonucleotide introduces a frameshift in the normal reading frame of the nucleotide sequence of interest.

20. (Previously presented) The method of claim 16, wherein the chimeric oligonucleotide introduces a premature stop codon in the normal reading frame of the nucleotide sequence of interest.

21. (Previously presented) The method of claim 16, wherein said nucleotide sequence of interest comprises a selectable marker.

22. (Previously presented) The method of claim 16, wherein said nucleotide sequence of interest modifies herbicide resistance.

23. (Previously presented) The method of claim 22, wherein said nucleotide sequence of interest encodes 5-enol pyruvylshikimate-3-phosphate synthase.

24. (Previously presented) The method of claim 22, wherein said nucleotide sequence of interest encodes acetohydroxy acid synthetase.

25. (Previously presented) The method of claim 23, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10.

26. (Previously presented) The method of claim 25, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 11, 12, and 13.

27. (Previously presented) The method of claim 16, wherein said plant is a monocot.

28. (Previously presented) The method of claim 27, wherein said monocot is maize.

29. (Previously presented) The method of claim 16, wherein said plant is a dicot.